

OM nucleic - nucleic search, using SW model

Run on: September 13, 2000, 10:17:53 ; Search time 1505.36 Seconds

(without alignments)  
1460.611 Million cell updates/sec

**Title:**

Perfect score:- 1232

Sequence: 1 gtcgaccacgcgtccgctc.....aaaaaaaaaaggcgccgc 1232

Scoring table: **IDENTITY\_NUC**

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters:	1945680
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Maximum DB seq length: 200000000000

Post-processing: Minimum Match 00

max/min match 100%  
Listing first 45 summaries

Database :

1:	gb_ba1.*
2:	gb_ba2.*
3:	gb_om.*
4:	gb_ov.*
5:	gb_pat.*
6:	gb_ph.*
7:	gb_p11.*
8:	gb_p12.*
9:	gb_p13.*
10:	gb_p14.*
11:	gb_p15.*
12:	gb_rto.*
13:	gb_sto.*
14:	gb_sy.*
15:	gb_un.*
16:	em_fun.*
17:	em_hum1.*
18:	em_hum2.*
19:	em_in.*
20:	em_om.*
21:	em_ov.*
22:	em_pat.*
23:	em_ph.*
24:	em_p11.*
25:	em_p12.*
26:	em_rto.*
27:	em_sto.*
28:	em_sy.*
29:	em_un.*
30:	em_vl.*
31:	gb_hg1.*
32:	gb_hg2.*
33:	gb_in1.*
34:	gb_in2.*
35:	em_ba1.*
36:	em_ba2.*
37:	em_hum3.*
38:	em_hum4.*
39:	gb_p14.*
40:	gb_hg3.*
41:	gb_hg4.*
42:	gb_hg5.*
43:	gb_hg6.*

44: em\_hcg7.\*  
45: em\_hcg1.\*  
46: em\_hcg2.\*  
47: em\_hcg3.\*  
48: em\_hcg4.\*  
49: pb.p15.\*  
50: pb.p13.\*  
51: pb\_hcg8.\*  
52: pb\_hcg9.\*  
53: pb\_hcg10.\*  
54: pb\_hcg11.\*  
55: pb\_hcg12.\*  
56: pb\_hcg13.\*  
57: pb\_hcg14.\*  
58: pb\_hcg15.\*  
59: pb\_hcg16.\*  
60: pb\_hcg17.\*  
61: pb\_hcg18.\*  
62: em\_hcg4.\*  
63: em\_hcg5.\*  
64: em\_hcg6.\*  
65: em\_hcg7.\*  
66: em\_hcg8.\*  
67: pb\_hcg1.\*  
68: pb\_hcg13.\*  
69: pb\_hcg12.\*  
70: pb\_hcg21.\*  
71: pb\_hcg22.\*  
72: pb\_hcg23.\*  
73: pb\_hcg24.\*  
74: pb\_hcg25.\*  
75: pb\_hcg27.\*  
76: pb\_hcg28.\*  
77: pb\_hcg28.\*  
78: pb\_hcg29.\*  
79: pb\_hcg31.\*  
80: pb\_hcg31.\*  
81: pb\_v12.\*  
82: pb\_v11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1201.6	97.5	199355	AC0160290	AC0160290	Hom sapi
2	258.4	21.0	127766	AC0057323	AC0057323	Hom sapi
3	258.4	21.0	158440	AC008437	AC008437	Hom sapi
4	252	20.5	177694	AC019358	AC019358	Hom sapi
5	252	20.5	168867	AP000902	AP000902	Hom sapi
6	251.6	20.4	155323	AC0090824	AC0090824	Hom sapi
7	250.6	20.3	99294	AC008704	AC008704	Hom sapi
8	250.6	20.3	118035	AC021852	AC021852	Hom sapi
9	250.6	20.3	119392	AC026620	AC026620	Hom sapi
10	250.6	20.3	165380	AC015941	AC015941	Hom sapi
11	250.2	20.3	134395	AC022290	AC022290	Hom sapi
12	250.2	20.3	201929	AL159177	AL159177	Hom sapi
13	249.4	20.2	139747	HS465N24	HS465N24	Hom sapi
14	249	20.2	135259	AC004590	AC004590	Human DNA
15	249	20.2	276336	AC011498	AC011498	Hom sapi
16	248.8	20.2	118555	HSJ908M14	HSJ908M14	Hom sapi
17	248.6	20.2	188165	AL119396	AL119396	Hom sapi
18	248.6	20.2	289755	AC020664	AC020664	Hom sapi
19	248.6	20.2	335668	AC021094	AC021094	Hom sapi
20	248.4	20.2	90832	AC003065	AC003065	Hom sapi
21	248.4	20.2	113843	AC005033	AC005033	Hom sapi
22	248.4	20.2	126228	AC006543	AC006543	Hom sapi
23	248.4	20.2	172010	AC026541	AC026541	Hom sapi
24	248.4	20.2	226916	AC005066	AC005066	Hom sapi



/note="assembly-fragment:01240  
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misc\_feature  
13415..24031  
/note="assembly-fragment:01322  
fragment\_chain:2"  
misc\_feature  
24132..28261  
/note="assembly-fragment:00061  
fragment\_chain:2"  
misc\_feature  
28362..31321  
/note="assembly-fragment:01050  
fragment\_chain:3"  
misc\_feature  
31422..37131  
/note="assembly-fragment:00450  
fragment\_chain:3"  
misc\_feature  
37232..40096  
/note="assembly-fragment:01049  
fragment\_chain:3"  
misc\_feature  
40197..43016  
/note="assembly-fragment:00600  
fragment\_chain:3"  
misc\_feature  
43117..44385  
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fragment\_chain:3"  
misc\_feature  
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misc\_feature  
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misc\_feature  
123997..129043  
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fragment\_chain:10"  
misc\_feature  
129144..132013  
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132114..138452  
/note="assembly-fragment:00481"  
138553..140132

/note="assembly-fragment:00813"  
140233..145011  
misc\_feature  
145112..146294  
/note="assembly-fragment:01075"  
146395..152223  
misc\_feature  
152324..156610  
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Query Match 97.5% Score 1201.6; DB 40; Length 199356;  
Best Local Similarity 99.7% Pred No. 0;  
Matches 1204; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 17 gctcagaagacccttgaatcacacagagattatataccagctcttcatgaagagccagcaa 76  
DB 33957 gctcagaagacccttgaatcacacagagattatataccagctcttcatgaagagccagcaa 34016  
QY 77 ccactggtcctatactgcttcttcccccacagactcaagcatcctcaggaagggaacc 136  
DB 34017 ccactggtcctatactgcttcttcccccacagactcaagcatcctcaggaagggaacc 34076  
QY 137 agaaacagagagaccatcttcaactgaagccttcccttctctctctctctctctctctct 196  
DB 34077 agaaacagagagaccatcttcaactgaagccttcccttctctctctctctctctctctct 34136  
QY 197 tccctgaagctgtctcaggttgagagcgaactgacacatccttgaacatggaacattact 256  
DB 34137 tccctgaagctgtctcaggttgagagcgaactgacacatccttgaacatggaacattact 34196  
QY 257 taacacagatgacacagaaacctgacatgctcccttctgaagctcccaatagtgacacacc 316  
DB 34197 taacacagatgacacagaaacctgacatgctcccttctgaagctcccaatagtgacacacc 34256  
QY 317 tctcaattgcccccaagaagaagagccctgagacacacagacatgacatctctgctgacacaaa 376  
DB 34257 tctcaattgcccccaagaagaagagccctgagacacacagacatgacatctctgctgacacaaa 34316  
QY 377 acagagatgctctcggagagaataatgaagagagaatttgctctgagccctggagcc 436  
DB 34317 acagagatgctctcggagagaataatgaagagagaatttgctctgagccctggagcc 34376  
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QY 497 gctggtgctatgacacagacacacacacacacacacacacacacacacacacacacacac 556  
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DB 34677 agtatcatcaccacacacacacacacacacacacacacacacacacacacacacacacacac 34736  
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DB 34737 tctggaagcaccatgacacacacacacacacacacacacacacacacacacacacacacacacac 34796  
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